FLUVIEW

A Weekly Influenza Surveillance Report Prepared by the Influenza Division

2016-2017 Influenza Season
Week 17 ending April 29, 2017

All data are preliminary and may change as more reports are received.

Synopsis: During week 17 (April 23-29, 2017), influenza activity decreased in the United States.

- **Viral Surveillance**: The most frequently identified influenza virus type reported by public health laboratories during week 17 was influenza B. The percentage of respiratory specimens testing positive for influenza in clinical laboratories decreased.
- **Novel Influenza A Virus**: One human infection with a novel influenza A virus was reported.
- **Pneumonia and Influenza Mortality**: The proportion of deaths attributed to pneumonia and influenza (P&I) was below the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System.
- **Influenza-associated Pediatric Deaths**: Ten influenza-associated pediatric deaths were reported, seven that occurred during the 2016-2017 season and three that occurred during the 2015-2016 season.
- **Influenza-associated Hospitalizations:** A cumulative rate for the season of 63.8 laboratory-confirmed influenza-associated hospitalizations per 100,000 population was reported.
- **Outpatient Illness Surveillance**: The proportion of outpatient visits for influenza-like illness (ILI) was 1.4%, which is below the national baseline of 2.2%. All ten regions reported ILI below their region-specific baseline levels. Four states experienced low ILI activity; New York City, Puerto Rico, and 46 states experienced minimal ILI activity; and the District of Columbia had insufficient data.
- **Geographic Spread of Influenza**: The geographic spread of influenza in three states was reported as widespread; Guam and eight states reported regional activity; the District of Columbia, Puerto Rico, and 20 states reported local activity; 19 states reported sporadic activity; and the U.S. Virgin Islands reported no activity.

National and Regional Summary of Select Surveillance Components

HHS Surveillance Regions*	Data for current week			Data cumulative since October 2, 2016 (week 40)						
	Out-patient ILI†	Number of jurisdictions reporting regional or widespread activity	% respiratory specimens positive for flu in clinical laboratories‡	A(H1N1) pdm09	A (H3)	A (Subtyping not performed)	B Victoria lineage	B Yamagata lineage	B lineage not performed	Pediatric Deaths
				Influenza test results from public health laboratories only						
Nation	Normal	12 of 54	6.9%	863	30,058	322	1,802	4,342	1,949	89
Region 1	Normal	5 of 6	17.7%	31	2,103	3	65	351	193	3
Region 2	Normal	2 of 4	12.0%	12	1,474	18	62	138	178	8
Region 3	Normal	0 of 6	10.4%	78	4,245	14	155	717	308	6
Region 4	Normal	1 of 8	11.3%	138	3,123	55	383	259	531	23
Region 5	Normal	1 of 6	10.7%	104	4,843	37	671	1,375	101	20
Region 6	Normal	0 of 5	7.5%	128	1,669	8	41	181	256	7
Region 7	Normal	0 of 4	5.6%	26	1,166	26	94	171	34	7
Region 8	Normal	0 of 6	6.8%	94	2,393	25	151	737	59	1
Region 9	Normal	2 of 5	6.0%	227	6,565	123	155	358	117	9
Region 10	Normal	1 of 4	6.2%	25	2,477	13	25	55	172	5

*http://www.hhs.gov/about/agencies/staff-divisions/iea/regional-offices/index.html
† Elevated means the % of visits for ILI is at or above the national or region-specific baseline.
§ Includes all 50 states, the District of Columbia, Guam, Puerto Rico, and the U.S. Virgin Islands
‡ National data are for current week; regional data are for the most recent three weeks.

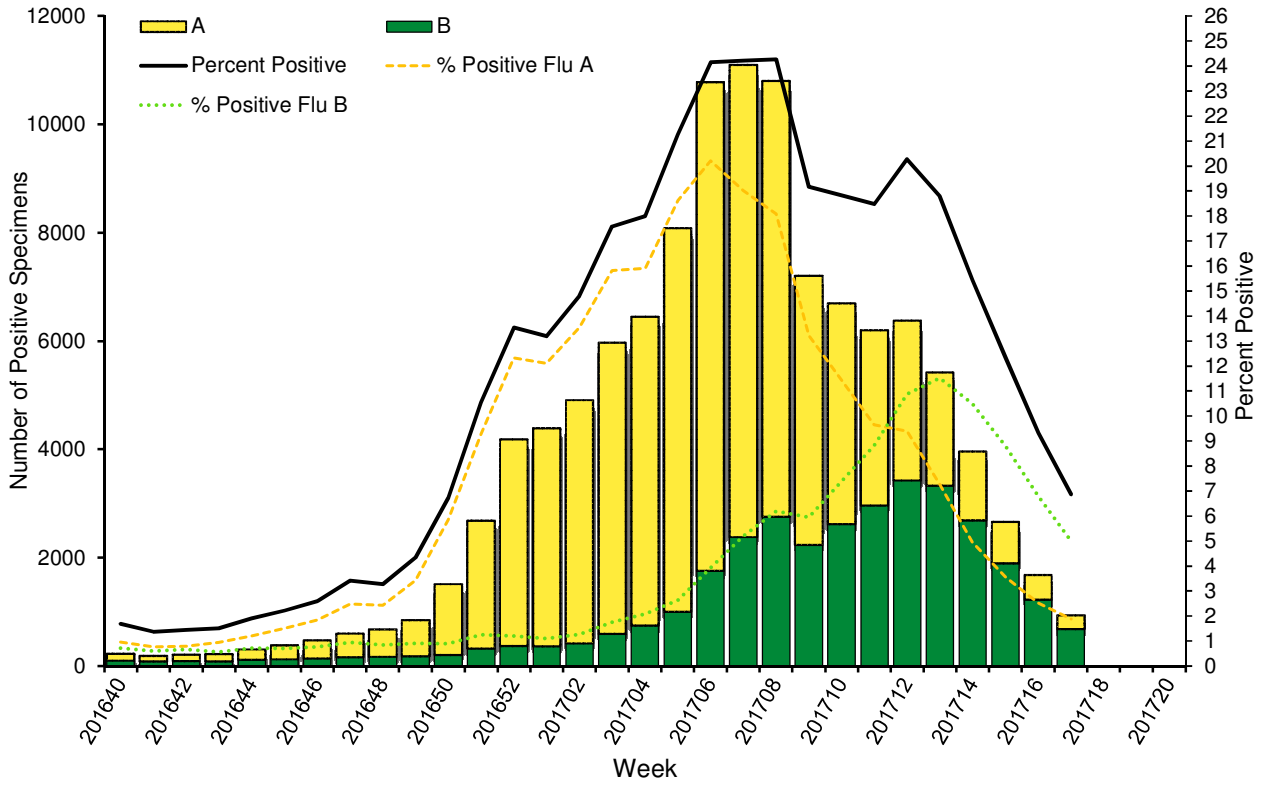
U.S. Virologic Surveillance: WHO and NREVSS collaborating laboratories, which include both public health and clinical laboratories located in all 50 states, Puerto Rico, and the District of Columbia, report to CDC the total number of respiratory specimens tested for influenza and the number positive for influenza by virus type. In addition, public health laboratories also report the influenza A subtype (H1 or H3) and influenza B lineage information for the viruses they test and the age or age group of the persons from whom the specimens were collected.

Additional virologic data can be found at: http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html and http://gis.cdc.gov/grasp/fluview/flu_by_age_virus.html.

The results of tests performed by clinical laboratories are summarized below.

	Week 17	Data Cumulative since October 2, 2016 (week 40)
No. of specimens tested	13,671	799,737
No. of positive specimens (%)	938 (6.9%)	116,139 (14.5%)
Positive specimens by type		
Influenza A	257 (27.4%)	82,911 (71.4%)
Influenza B	681 (72.6%)	33,228 (28.6%)

Influenza Positive Tests Reported to CDC by U.S. Clinical Laboratories, National Summary, 2016-2017 Season

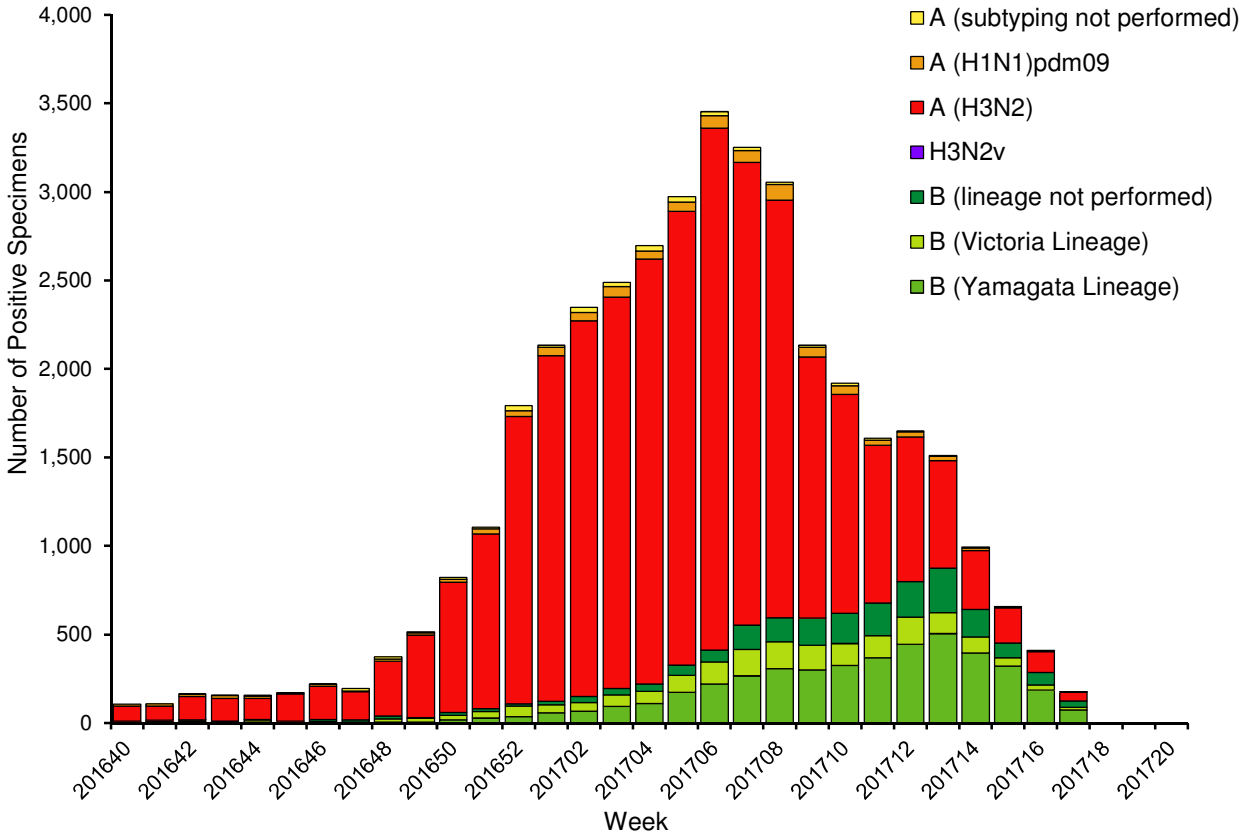


The results of tests performed by public health laboratories, as well as the age group distribution of influenza positive tests, are summarized below.

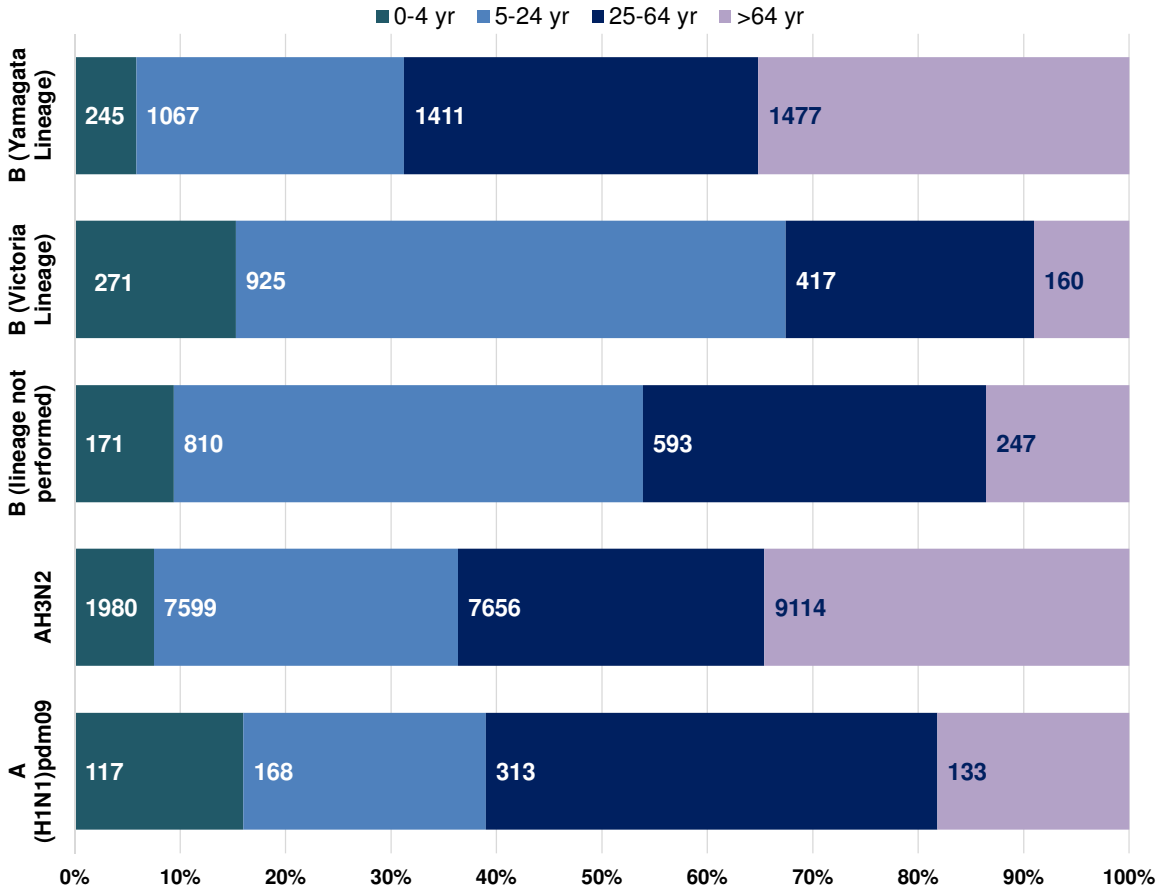
	Week 17	Data Cumulative since October 2, 2016 (week 40)
No. of specimens tested	593	80,341
No. of positive specimens*	177	39,336
Positive specimens by type/subtype		
Influenza A	52 (29.4%)	31,243 (79.4%)
A(H1N1)pdm09	2 (3.8%)	863 (2.8%)
H3	48 (92.3%)	30,058 (96.2%)
Subtyping not performed	2 (3.8%)	322 (1.0%)
Influenza B	125 (70.6%)	8,093 (20.6%)
Yamagata lineage	74 (59.2%)	4,342 (53.7%)
Victoria lineage	15 (12.0%)	1,802 (22.3%)
Lineage not performed	36 (28.8%)	1,949 (24.1%)

*The percent of specimens testing positive for influenza is not reported because public health laboratories often receive samples that have already tested positive for influenza at a clinical laboratory and therefore percent positive would not be a valid indicator of influenza activity. Additional information is available at http://www.cdc.gov/flu/weekly/overview.htm

Influenza Positive Tests Reported to CDC by U.S. Public Health Laboratories, National Summary, 2016-2017 Season



Age Group Proportions and Total by Influenza Subtype Reported by Public Health Laboratories, 2016-2017 Season



Novel Influenza A Virus: One human infection with a novel influenza A virus was reported by the state of Texas. The person was infected with an influenza A (H3N2) variant (H3N2v) virus. This H3N2v virus was detected through the Department of Defense Global, Laboratory-based Influenza Surveillance Program. The patient became ill with respiratory symptoms in February 2017, was not hospitalized, and has fully recovered from their illness. Swine contact at an agricultural event was reported in the week preceding illness onset. This is the first H3N2v virus infection detected in the United States in 2017.

Influenza viruses that circulate in swine are called swine influenza viruses when isolated from swine, but are called variant influenza viruses when isolated from humans. Early identification and investigation of human infections with novel influenza A viruses are critical so that the risk of infection can be more fully understood and appropriate public health measures can be taken. Additional information on influenza in swine, variant influenza infection in humans, and strategies to interact safely with swine can be found at http://www.cdc.gov/flu/swineflu/index.htm.

Influenza Virus Characterization: CDC characterizes influenza viruses through one or more tests including genomic sequencing, hemagglutination inhibition (HI) and/or neutralization assays. These data are used to compare how similar currently circulating influenza viruses are to the reference viruses used for developing influenza vaccines, and to monitor for changes in circulating influenza viruses. Historically, HI data have been used most commonly to assess the similarity between reference viruses and circulating viruses to suggest how well the vaccine may work until such a time as vaccine effectiveness estimates are available.

For nearly all virus positive surveillance samples received at CDC, next-generation sequencing is performed to ascertain genomic data of circulating influenza viruses. Viruses can be classified into genetic groups/clades based on analysis of their HA gene segments using phylogenetics and key amino acid changes (Klimov Vaccine 2012).

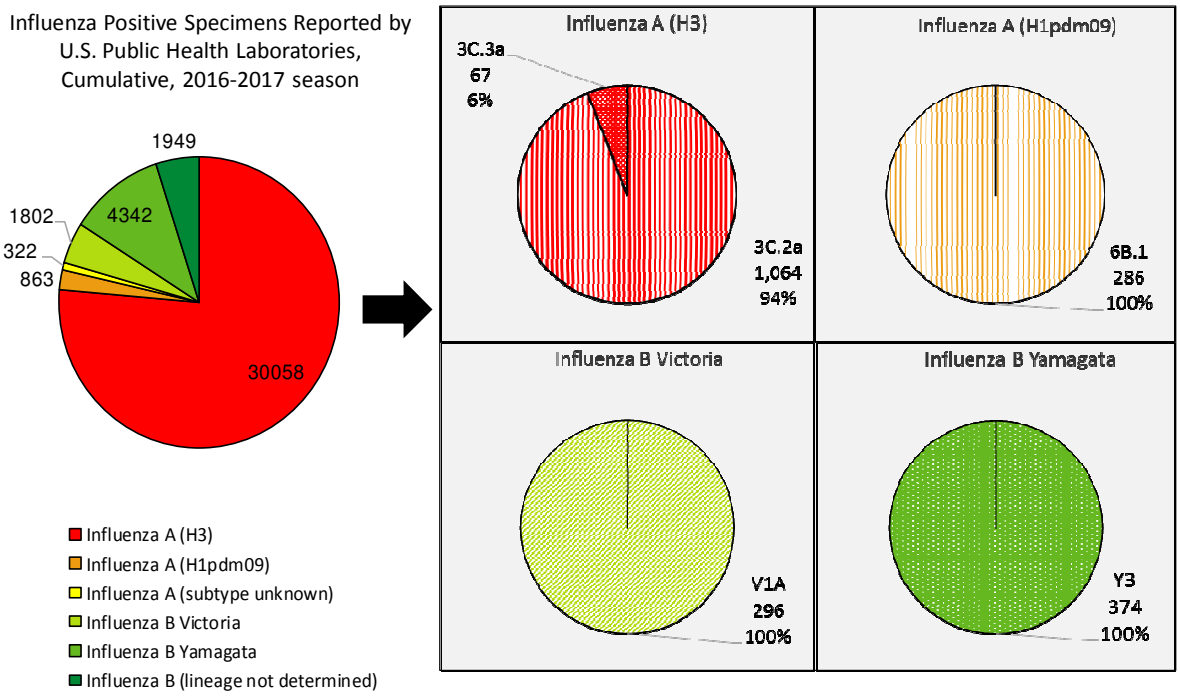
A proportion of influenza A (H3N2) viruses do not yield sufficient hemagglutination titers for antigenic characterization using the hemagglutination inhibition test. Therefore, CDC selects a subset of influenza A (H3N2) viruses to test using a focus reduction assay for supplementary antigenic characterization.

Genetic Characterization

During the 2016-2017 season, 39,336 influenza positive specimens have been collected and reported by public health laboratories in the United States (Figure, left). CDC genetically characterized 2,087 influenza viruses [286 influenza A (H1N1)pdm09, 1,131 influenza A (H3N2), and 670 influenza B viruses] collected by U.S. laboratories. The HA gene segment of all influenza A (H1N1)pdm09 viruses analyzed belonged to genetic group 6B.1. Influenza A (H3N2) virus HA gene segments analyzed belonged to genetic groups 3C.2a or 3C.3a. Genetic group 3C.2a includes a newly emerging subgroup known as 3C.2a1. The HA of influenza B/Victoria-lineage viruses all belonged to genetic group V1A. The HA of influenza B/Yamagata-lineage viruses analyzed all belonged to genetic group Y3.

The majority of U.S. viruses submitted for characterization come from state and local public health laboratories. Due to Right Size Roadmap considerations, specimen submission guidance issued to the laboratories request that, if available, 2 influenza A (H1N1), 2 influenza A (H3N2), and 2 influenza B viruses be submitted every other week. Because of this, the number of each virus type/subtype characterized should be approximately equal. In the figure below, the results of tests performed by public health labs are presented on the left and sequence results by genetic group of specimens submitted to CDC are presented on the right.

Sequence Results, by Genetic Group, of Specimens Submitted to CDC by U.S. Public Health Laboratories, Cumulative, 2016-2017 season



Antigenic Characterization: CDC has antigenically characterized 1,577 influenza viruses [259 influenza A (H1N1)pdm09, 679 influenza A (H3N2), and 639 influenza B viruses] collected by U.S. laboratories since October 1, 2016.

Influenza A Virus [938]

A (H1N1)pdm09 [259]: 257 of 259 (99.2%) influenza A (H1N1)pdm09 viruses were antigenically characterized using ferret post-infection antisera as A/California/7/2009-like, the influenza A (H1N1) component of the 2016-2017 Northern Hemisphere vaccine.

A (H3N2) [679]: 652 of 679 (96.0%) influenza A (H3N2) viruses were antigenically characterized as A/Hong Kong/4801/2014-like, a virus that belongs in genetic group 3C.2a and is the influenza A (H3N2) component of the 2016-2017 Northern Hemisphere vaccine, by HI testing or neutralization testing. Among the viruses which reacted poorly with ferret antisera raised against A/Hong Kong/4801/2014-like viruses, 23 out of 27 (85.2%) are more closely related to A/Switzerland/9715293/2013, a virus belonging to genetic group 3C.3a.

Influenza B Virus [639]

Victoria Lineage [278]: 249 of 278 (89.6%) B/Victoria-lineage viruses were antigenically characterized using ferret post-infection antisera as B/Brisbane/60/2008-like, which is included as an influenza B component of the 2016-2017 Northern Hemisphere trivalent and quadrivalent influenza vaccines.

Yamagata Lineage [361]: All 361 (100%) B/Yamagata-lineage viruses were antigenically characterized using ferret post-infection antisera as B/Phuket/3073/2013-like, which is included as an influenza B component of the 2016-2017 Northern Hemisphere quadrivalent influenza vaccines.

2017-2018 Influenza Season – U.S. Influenza Vaccine Composition: The World Health Organization (WHO) has recommended the Northern Hemisphere 2017-2018 influenza vaccine composition, and the Food and Drug Administration's Vaccines and Related Biological Products Advisory Committee (VRBPAC) subsequently made the influenza vaccine composition recommendation for the United States. Both agencies recommend that trivalent vaccines contain an A/Michigan/45/2015 (H1N1)pdm09-like virus, an A/Hong Kong/4801/2014 (H3N2)-like virus, and a B/Brisbane/60/2008-like (B/Victoria lineage) virus. It is recommended that quadrivalent vaccines, which have two influenza B viruses, contain the viruses recommended for the trivalent vaccines, as well as a B/Phuket/3073/2013-like (B/Yamagata lineage) virus. This is the same recommendation made for the 2017 Southern Hemisphere vaccines, but it does represent an update to the influenza A (H1N1) component recommended for 2016-2017 Northern Hemisphere influenza vaccines. These vaccine recommendations were based on several factors, including global influenza virologic and epidemiologic surveillance, genetic characterization, antigenic characterization, antiviral resistance, and the candidate vaccine viruses that are available for production.

Antiviral Resistance: Testing of influenza A (H1N1)pdm09, influenza A (H3N2), and influenza B virus isolates for resistance to neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir) is performed at CDC using a functional assay. Additional influenza A (H1N1)pdm09 and influenza A (H3N2) viruses from clinical samples are tested for mutations known to confer oseltamivir resistance. The data summarized below combine the results of both testing methods. These samples are routinely obtained for surveillance purposes rather than for diagnostic testing of patients suspected to be infected with antiviral-resistant virus.

High levels of resistance to the adamantanes (amantadine and rimantadine) persist among influenza A (H1N1)pdm09 and influenza A (H3N2) viruses (the adamantanes are not effective against influenza B viruses). Therefore, data from adamantane resistance testing are not presented below.

Neuraminidase Inhibitor Resistance Testing Results on Samples Collected Since October 1, 2016

	Oseltamivir		Zanamivir		Peramivir	
	Virus Samples tested (n)	**Resistant Viruses, Number (%)**	**Virus Samples tested (n)**	**Resistant Viruses, Number (%)**	**Virus Samples tested (n)**	**Resistant Viruses, Number (%)**
Influenza A (H1N1)pmd09	296	0 (0.0)	282	0 (0.0)	296	0 (0.0)
Influenza A (H3N2)	2,099	0 (0.0)	2,099	0 (0.0)	1,197	0 (0.0)
Influenza B	728	0 (0.0)	728	0 (0.0)	728	0 (0.0)

The majority of recently circulating influenza viruses are susceptible to the neuraminidase inhibitor antiviral medications, oseltamivir, zanamivir, and peramivir; however, rare sporadic instances of oseltamivir-resistant and peramivir-resistant influenza A (H1N1)pdm09 viruses and oseltamivir-

resistant influenza A (H3N2) viruses have been detected worldwide. Antiviral treatment as early as possible is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at high risk for serious influenza-related complications. Additional information on recommendations for treatment and chemoprophylaxis of influenza virus infection with antiviral agents is available at http://www.cdc.gov/flu/antivirals/index.htm.

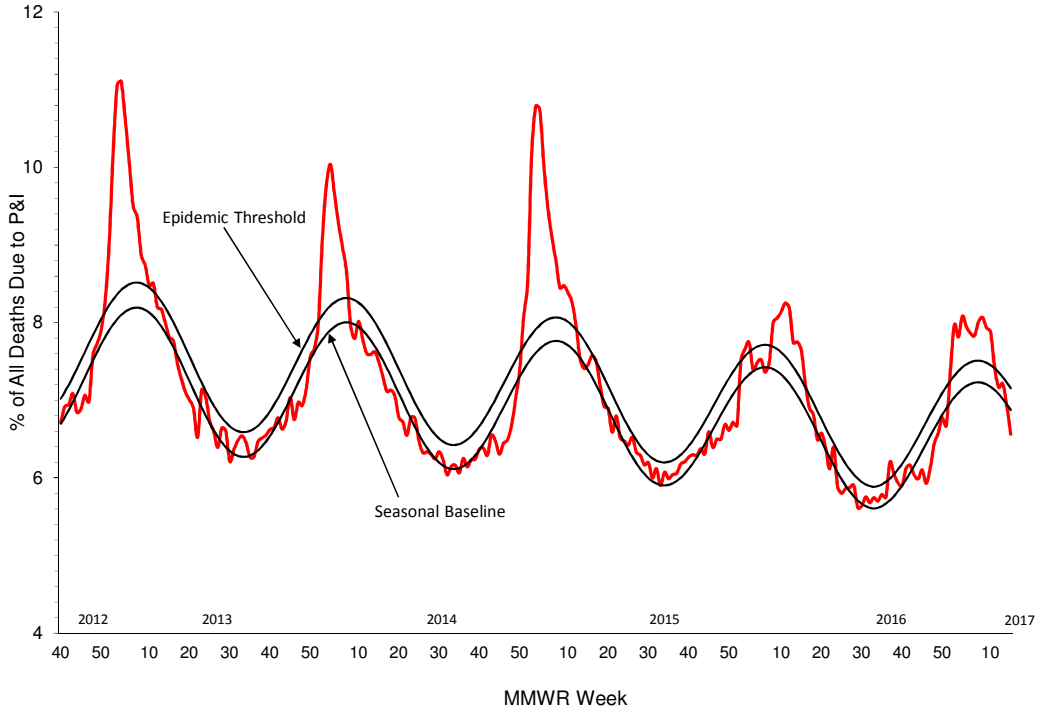
Pneumonia and Influenza (P&I) Mortality Surveillance: Based on National Center for Health Statistics (NCHS) mortality surveillance data available on May 4, 2017, 6.6% of the deaths occurring during the week ending April 15, 2017 (week 15) were due to P&I. This percentage is below the epidemic threshold of 7.2% for week 15.

Background: Weekly mortality surveillance data include a combination of machine coded and manually coded causes of death collected from death certificates. There is a backlog of data requiring manual coding within NCHS mortality surveillance data. The percentages of deaths due to P&I are higher among manually coded records than more rapidly available machine coded records and may result in initially reported P&I percentages that are lower than percentages calculated from final data. Efforts continue to reduce and monitor the number of records awaiting manual coding.

Beginning in the week ending October 8, 2016 (week 40), CDC retired the 122 Cities Mortality Reporting System and uses only the NCHS Mortality Surveillance System.

Region and state-specific data are available at http//gis.cdc.gov/grasp/fluview/mortality.html.

Pneumonia and Influenza Mortality from
the National Center for Health Statistics Mortality Surveillance System
Data through the week ending April 15, 2017, as of May 4, 2017

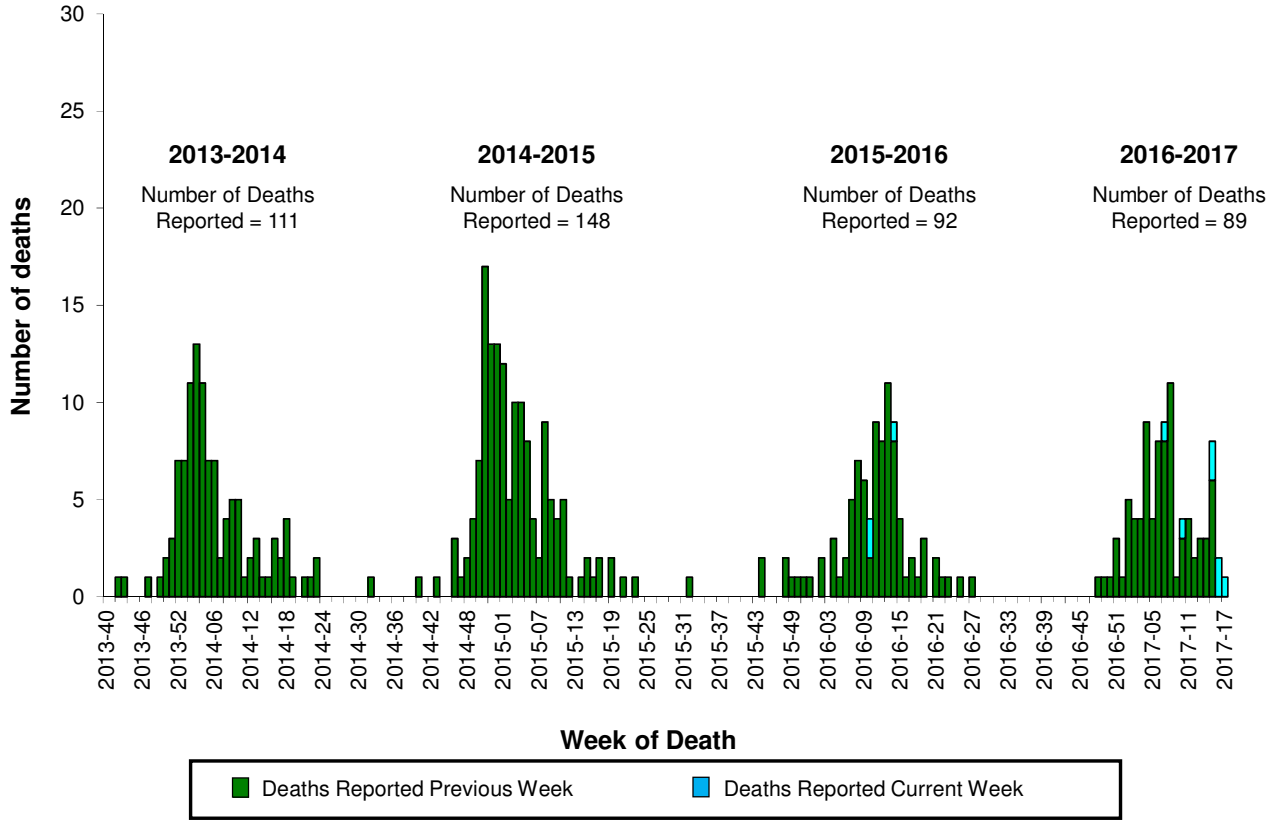


Influenza-Associated Pediatric Mortality: Ten influenza-associated pediatric deaths were reported to CDC during week 17. One death was associated with an influenza A (H3) virus and occurred during week 17 (the week ending April 29, 2017). One death was associated with an influenza A virus for which no subtyping was performed and occurred during week 10 (the week ending March 11, 2017). Five deaths were associated with an influenza B virus and occurred during weeks 7, 15, and 16 (the weeks ending February 18, April 15, and April 22, 2017, respectively). One death that was reported earlier this season was reclassified by the reporting jurisdiction. A total of 89 influenza-associated pediatric deaths have been reported for the 2016-2017 season.

Three influenza-associated pediatric deaths that occurred during the 2015-2016 season were reported to CDC. One death was associated with an influenza A (H1N1)pdm09 virus, one was associated with an influenza A virus for which no subtyping was performed, and one was associated with an influenza B virus. This brings the total number of reported influenza-associated pediatric deaths occurring during that season to 92.

Additional data can be found at: http://gis.cdc.gov/GRASP/Fluview/PedFluDeath.html.

Number of Influenza-Associated Pediatric Deaths by Week of Death: 2013-2014 season to present



Influenza-Associated Hospitalizations: The Influenza Hospitalization Surveillance Network (FluSurv-NET) conducts population-based surveillance for laboratory-confirmed influenza-related hospitalizations in children younger than 18 years of age (since the 2003-2004 influenza season) and adults (since the 2005-2006 influenza season).

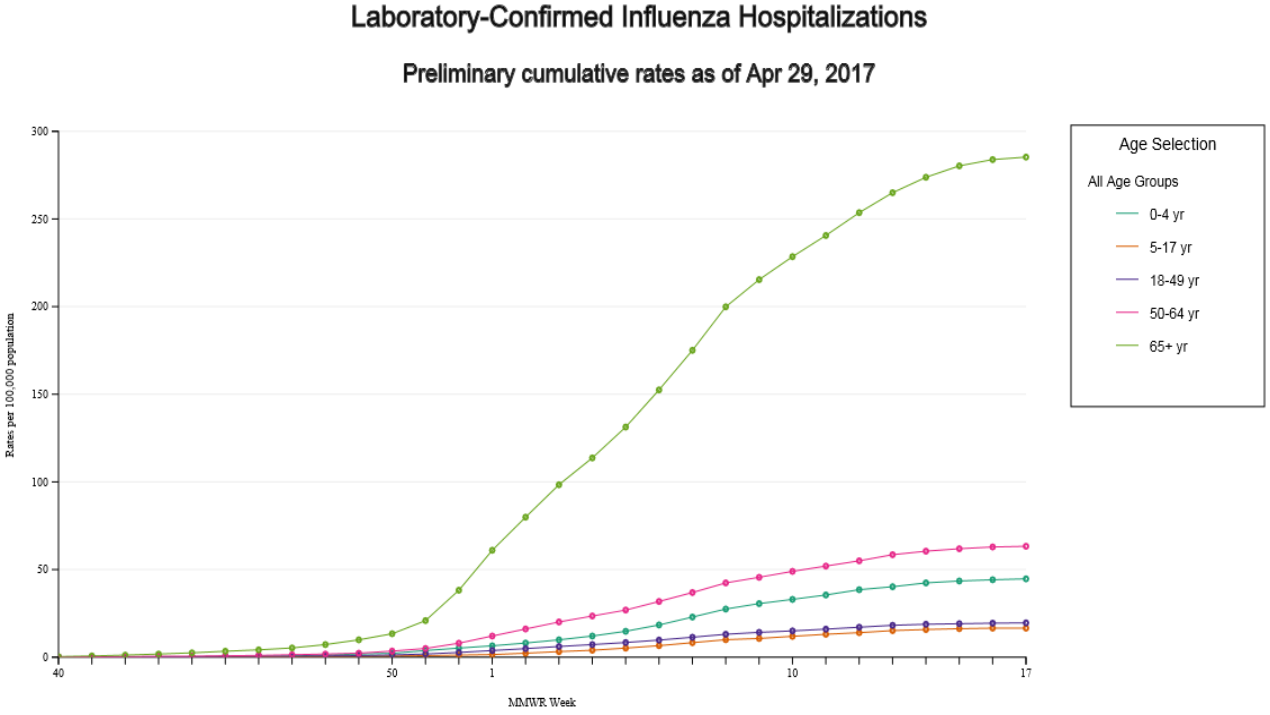
The FluSurv-NET covers more than 70 counties in the 10 Emerging Infections Program (EIP) states (CA, CO, CT, GA, MD, MN, NM, NY, OR, and TN) and additional Influenza Hospitalization Surveillance Project (IHSP) states. The IHSP began during the 2009-2010 season to enhance surveillance during the 2009 H1N1 pandemic. IHSP sites included IA, ID, MI, OK and SD during the 2009-2010 season; ID, MI, OH, OK, RI, and UT during the 2010-2011 season; MI, OH, RI, and UT during the 2011-2012 season; IA, MI, OH, RI, and UT during the 2012-2013 season; and MI, OH, and UT during the 2013-2014, 2014-2015, 2015-2016, and 2016-2017 seasons.

Data gathered are used to estimate age-specific hospitalization rates on a weekly basis and describe characteristics of persons hospitalized with severe influenza illness. The rates provided are likely to be an underestimate as influenza-related hospitalizations can be missed, either because testing is not performed, or because cases may be attributed to other causes of pneumonia or other common influenza-related complications.

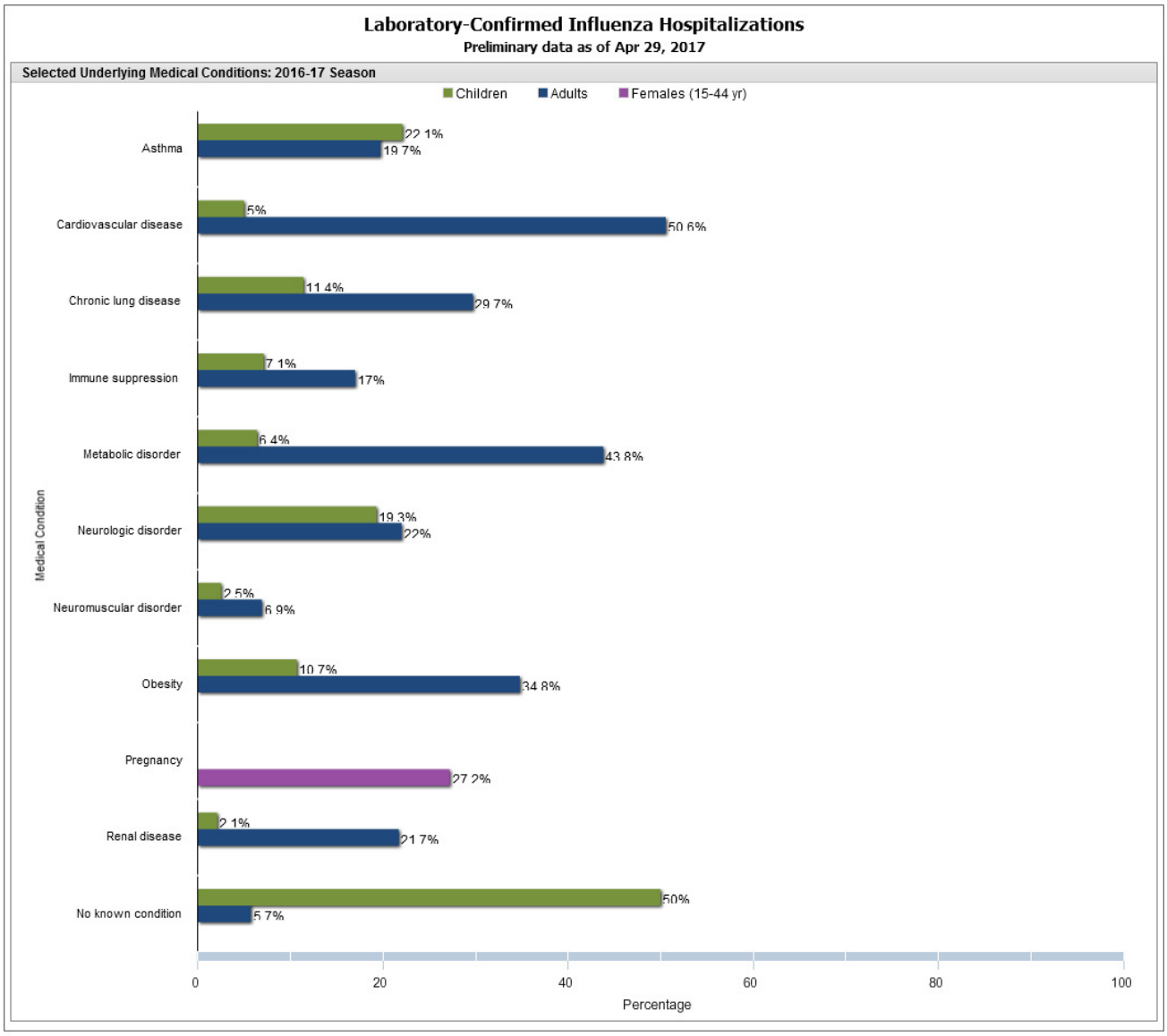
Between October 1, 2016 and April 29, 2017, 17,871 laboratory-confirmed influenza-associated hospitalizations were reported. The overall hospitalization rate was 63.8 per 100,000 population. The highest rate of hospitalization was among adults aged ≥65 years (285.3 per 100,000 population), followed by adults aged 50-64 (63.3 per 100,000 population) and children aged 0-4 years (44.7 per 100,000 population). Among 17,871 hospitalizations, 14,050 (78.6%) were associated with influenza A virus, 3,689 (20.6%) with influenza B virus, 58 (0.3%) with influenza A virus and influenza B virus co-infection, and 74 (0.4%) with influenza virus for which the type was not determined. Among those with influenza A subtype information, 5,025 (98.0%) were A(H3N2) and 105 (2.0%) were A(H1N1)pdm09 virus.

Clinical findings are preliminary and based on 4,326 (24.2%) cases with complete medical chart abstraction. Among 4,046 hospitalized adults with complete medical chart abstraction, 3,816 (94.3%) had at least one reported underlying medical condition; the most commonly reported were cardiovascular disease, metabolic disorders, obesity and chronic lung disease. Among 280 hospitalized children with complete medical chart abstraction, 139 (49.6%) had at least one underlying medical condition; the most commonly reported were asthma, neurologic disorder, chronic lung disease, and obesity. Among the 276 hospitalized women of childbearing age (15-44 years), 75 (27.2%) were pregnant.

Additional FluSurv-NET data can be found at: http://gis.cdc.gov/GRASP/Fluview/FluHospRates.html and http://gis.cdc.gov/grasp/fluview/FluHospChars.html.



Data are from the Influenza Hospitalization Surveillance Network (FluSurv-NET), a population-based surveillance for influenza related hospitalizations in children and adults in 13 U.S. states. Incidence rates are calculated using the National Center for Health Statistics' (NCHS) population estimates for the counties included in the surveillance catchment area.

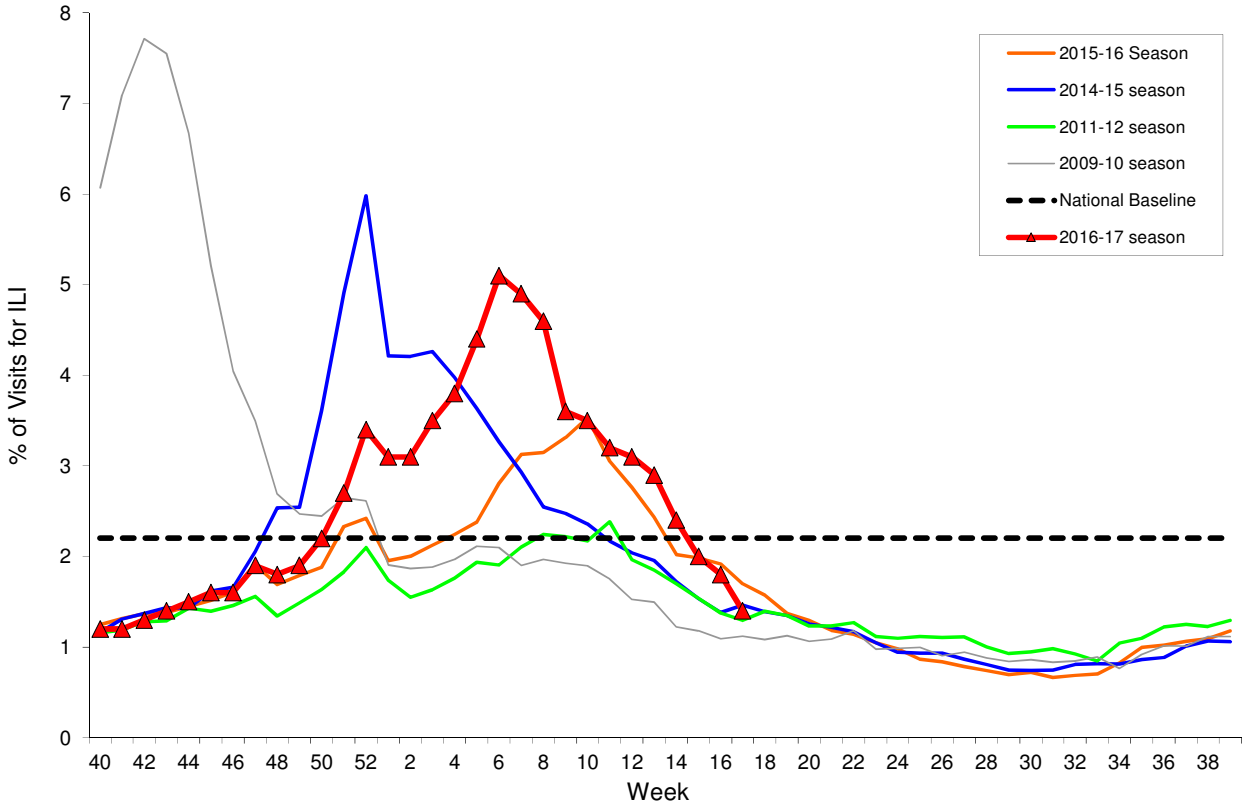


FluSurv-NET data are preliminary and displayed as they become available. Therefore, figures are based on varying denominators as some variables represent information that may require more time to be collected. Data are refreshed and updated weekly. Asthma includes a medical diagnosis of asthma or reactive airway disease; Cardiovascular diseases include conditions such as coronary heart disease, cardiac valve disorders, congestive heart failure, and pulmonary hypertension; does not include isolated hypertension; Chronic lung diseases include conditions such as chronic obstructive pulmonary disease, bronchiolitis obliterans, chronic aspiration pneumonia, and interstitial lung disease; Immune suppression includes conditions such as immunoglobulin deficiency, leukemia, lymphoma, HIV/AIDS, and individuals taking immunosuppressive medications; Metabolic disorders include conditions such as diabetes mellitus; Neurologic diseases include conditions such as seizure disorders, cerebral palsy, and cognitive dysfunction; Neuromuscular diseases include conditions such as multiple sclerosis and muscular dystrophy; Obesity was assigned if indicated in patient's medical chart or if body mass index (BMI) >30 kg/m^2; Pregnancy percentage calculated using number of influenza-positive females aged between 15 and 44 years of age as the denominator; Renal diseases include conditions such as acute or chronic renal failure, nephrotic syndrome, glomerulonephritis, and impaired creatinine clearance; No known condition indicates that the person did not have any known high risk medical condition indicated in medical chart at the time of hospitalization.

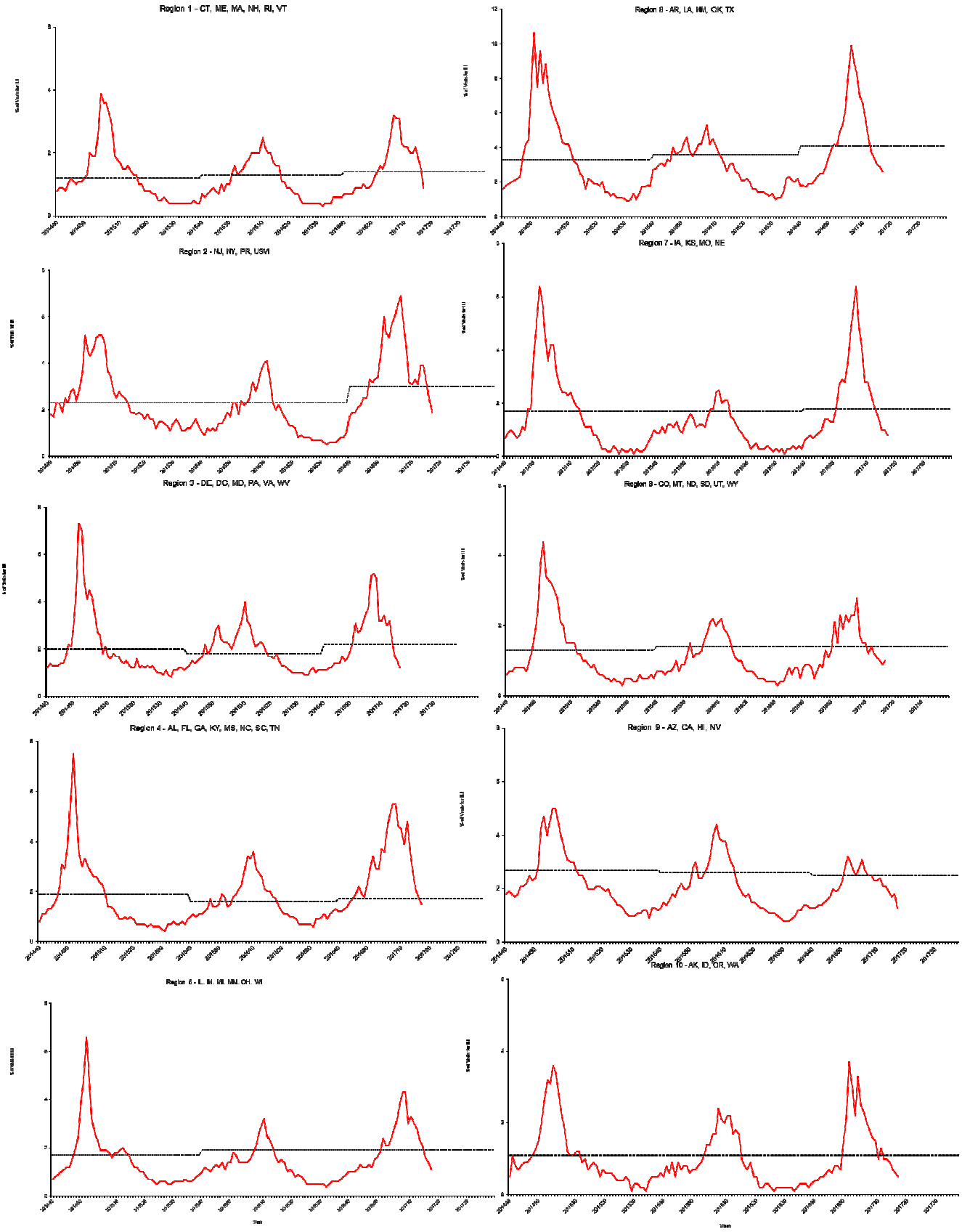
Outpatient Illness Surveillance: Nationwide during week 17, 1.4% of patient visits reported through the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) were due to influenza-like illness (ILI). This percentage is below the national baseline of 2.2%. *(ILI is defined as fever (temperature of 100°F [37.8°C] or greater) and cough and/or sore throat.)*

Additional data are available at http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html.

Percentage of Visits for Influenza-like Illness (ILI) Reported by the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet), Weekly National Summary, 2016-2017 and Selected Previous Seasons



On a regional level, the percentage of outpatient visits for ILI ranged from 0.5% to 2.6% during week 17. All 10 regions reported a proportion of outpatient visits for ILI below their region-specific baseline levels.



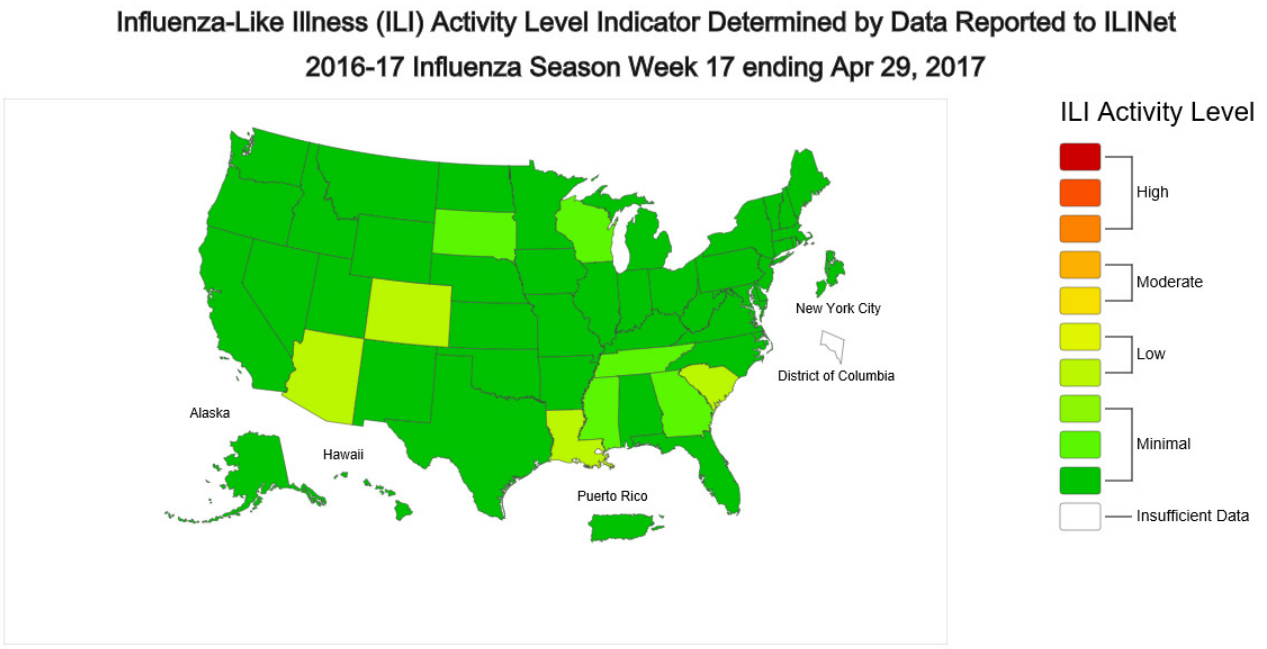
NOTE: Scales differ between regions. Regional baselines are calculated each influenza season and may differ from season to season.

*Use of the regional baselines for state data is not appropriate.

ILINet State Activity Indicator Map: Data collected in ILINet are used to produce a measure of ILI activity* by state. Activity levels are based on the percent of outpatient visits in a state due to ILI and are compared to the average percent of ILI visits that occur during weeks with little or no influenza virus circulation. Activity levels range from minimal, which would correspond to ILI activity from outpatient clinics being below, or only slightly above, the average, to high, which would correspond to ILI activity from outpatient clinics being much higher than average.

During week 17, the following ILI activity levels were experienced:

- Four states (Arizona, Colorado, Louisiana, and South Carolina) experienced low ILI activity.
- New York City, Puerto Rico, and 46 states (Alabama, Alaska, Arkansas, California, Connecticut, Delaware, Florida, Georgia, Hawaii, Idaho, Illinois, Indiana, Iowa, Kansas, Kentucky, Maine, Maryland, Massachusetts, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, Nevada, New Hampshire, New Jersey, New Mexico, New York, North Carolina, North Dakota, Ohio, Oklahoma, Oregon, Pennsylvania, Rhode Island, South Dakota, Tennessee, Texas, Utah, Vermont, Virginia, Washington, West Virginia, Wisconsin, and Wyoming) experienced minimal ILI activity.
- Data were insufficient to calculate an ILI activity level from the District of Columbia.



*This map uses the proportion of outpatient visits to health care providers for influenza-like illness to measure the ILI activity level within a state. It does not, however, measure the extent of geographic spread of flu within a state. Therefore, outbreaks occurring in a single city could cause the state to display high activity levels.

Data collected in ILINet may disproportionally represent certain populations within a state, and therefore, may not accurately depict the full picture of influenza activity for the whole state.

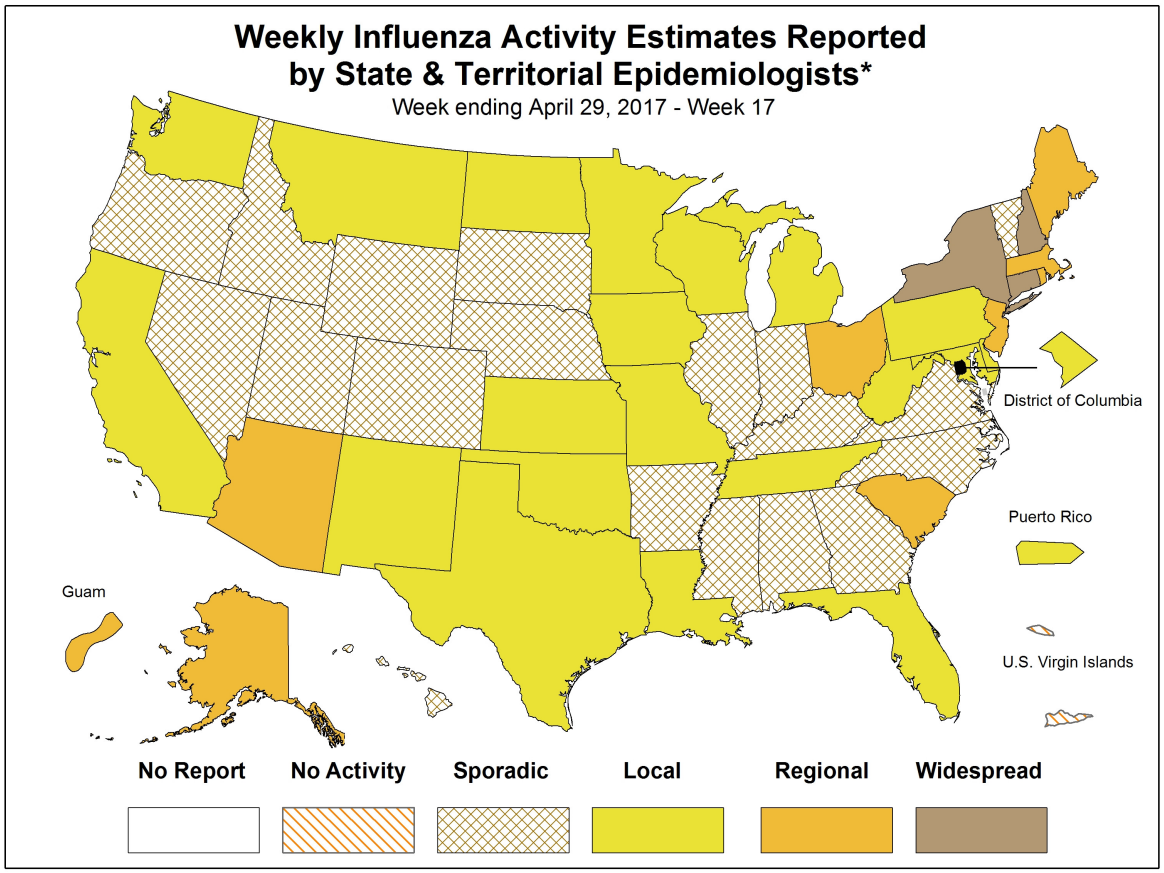
Data displayed in this map are based on data collected in ILINet, whereas the State and Territorial flu activity map is based on reports from state and territorial epidemiologists. The data presented in this map are preliminary and may change as more data are received. Differences in the data presented here by CDC and independently by some state health departments likely represent differing levels of data completeness with data presented by the state likely being the more complete.

Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists: The influenza activity reported by state and territorial epidemiologists indicates geographic spread of influenza viruses, but does not measure the severity of influenza activity.

Additional data are available at: https://gis.cdc.gov/grasp/fluview/FluView8.html.

During week 17, the following influenza activity was reported:

- Widespread influenza activity was reported by three states (Connecticut, New Hampshire, and New York).
- Regional influenza activity was reported by Guam and eight states (Alaska, Arizona, Maine, Massachusetts, New Jersey, Ohio, Rhode Island, and South Carolina).
- Local influenza activity was reported by the District of Columbia, Puerto Rico, and 20 states (California, Delaware, Florida, Iowa, Kansas, Louisiana, Maryland, Michigan, Minnesota, Missouri, Montana, New Mexico, North Dakota, Oklahoma, Pennsylvania, Tennessee, Texas, Washington, West Virginia, and Wisconsin,).
- Sporadic activity was reported by 19 states (Alabama, Arkansas, Colorado, Georgia, Hawaii, Idaho, Illinois, Indiana, Kentucky, Mississippi, Nebraska, Nevada, North Carolina, Oregon, South Dakota, Utah, Vermont, Virginia and Wyoming).
- No influenza activity was reported by the U.S. Virgin Islands.



* This map indicates geographic spread & does not measure the severity of influenza activity

Additional National and International Influenza Surveillance Information

FluView Interactive: FluView includes enhanced web-based interactive applications that can provide dynamic visuals of the influenza data collected and analyzed by CDC. These FluView Interactive applications allow people to create customized, visual interpretations of influenza data, as well as make comparisons across flu seasons, regions, age groups and a variety of other demographics. To access these tools, visit http://www.cdc.gov/flu/weekly/fluviewinteractive.htm.

U.S. State, territorial, and local influenza surveillance: Click on a jurisdiction below to access the latest local influenza information.

Alabama	Alaska	Arizona	Arkansas	California
Colorado	Connecticut	Delaware	District of Columbia	Florida
Georgia	Hawaii	Idaho	Illinois	Indiana
Iowa	Kansas	Kentucky	Louisiana	Maine
Maryland	Massachusetts	Michigan	Minnesota	Mississippi
Missouri	Montana	Nebraska	Nevada	New Hampshire
New Jersey	New Mexico	New York	North Carolina	North Dakota
Ohio	Oklahoma	Oregon	Pennsylvania	Rhode Island
South Carolina	South Dakota	Tennessee	Texas	Utah
Vermont	Virginia	Washington	West Virginia	Wisconsin
Wyoming	New York City	Puerto Rico	U.S. Virgin Islands	

World Health Organization: Additional influenza surveillance information from participating WHO member nations is available through FluNet and the Global Epidemiology Reports.

WHO Collaborating Centers for Influenza located in Australia, China, Japan, the United Kingdom, and the United States (CDC in Atlanta, Georgia).

Europe: For the most recent influenza surveillance information from Europe, please see WHO/Europe and the European Centre for Disease Prevention and Control at http://www.flunewseurope.org/

Public Health Agency of Canada: The most up-to-date influenza information from Canada is available at http://www.phac-aspc.gc.ca/fluwatch/.

Public Health England: The most up-to-date influenza information from the United Kingdom is available at https://www.gov.uk/government/statistics/weekly-national-flu-reports.

Any links provided to non-Federal organizations are provided solely as a service to our users. These links do not constitute an endorsement of these organizations or their programs by CDC or the Federal Government, and none should be inferred. CDC is not responsible for the content of the individual organization web pages found at these links.

An overview of the CDC influenza surveillance system, including methodology and detailed descriptions of each data component, is available at: http://www.cdc.gov/flu/weekly/overview.htm.

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